SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Blackburn, Michael
 Church, William
 Gross, Mitchell
 Feuerstein, Giora
 Nichols, Andrew
 Padlan, Eduardo
 Patel, Arunbhai
 Sylvester, Daniel
- (ii) TITLE OF THE INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT OF THROMBOSIS
 - (iii) NUMBER OF SEQUENCES: 111
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: SmithKline Beecham Corporation
 - (B) STREET: 709 Swedeland Road
 - (C) CITY: King of Prussia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19406
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 16-JAN-1997
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/029,119
 - (B) FILING DATE: 24-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Baumeister, Kirk
- (B) REGISTRATION NUMBER: 33,833
- (C) REFERENCE/DOCKET NUMBER: P50438
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 610-270-5096
 - (B) TELEFAX:
 - (C) TELEX:
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CATCCTAGAG TCACCGAGGA

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
AGCTGCCCAA AGTGCCCAAG C	21
(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 36 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG	36
(2) INFORMATION FOR SEQ ID NO:4:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
GATTTTCARG TGCAGATTTT C	21

(2) INFORMATION FOR SEQ ID NO:5:

(i)	SECUENCE	CHARACTERISTICS
1 1 1		CITATO L DICE DE L'OC

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGATCCAGT	TGGTGCAGTC	TGGACCTGAG	CTGAAGAAGC	CTGGAGAGAC	AGTCAAGATC	60
TCCTGCAAGG	CTTCTGGGTA	CACCTTCACA	AACTATGGAA	${\tt TGAACTGGGT}$	GAAGCAGGCT	120
CCAGGAAAGG	GTTTAAAGTG	GATGGGCTGG	ATAAACACCA	GAAATGGAAA	GTCAACATAT	180
GTTGATGACT	TCAAGGGACG	GTTTGCCTTC	TCTTTGGAAA	GCTCTGCCAG	CACTGCCAAT	240
TTGCAGATCG	ACAACCTCAA	AGATGAGGAC	ACGGCTACAT	ATTTCTGTAC	AAGAGAAGGG	300
AATATGGATG	GTTACTTCCC	TTTTACTTAC	TGGGGCCAAG	$\operatorname{GGACTCTGGT}$	CACTGTCTCT	360
GCA						363

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAAATTGTTC	TCTCCCAGTC	TCCAGCAATC	CTGTCTGCAT	CTCCAGGGGA	GAAGGTCACA	60
ATGACTTGCA	GGGCCAGCTC	AAGTGTAAAT	TACATGCACT	GGTACCAGCA	GAAGCCAGGA	120
TCCTCCCCCA	AACCCTGGAT	TTATGCCACA	TCCAACCTGG	${\tt CTTCTGGAGT}$	CCCTGCTCGC	180
TTCAGTGGCA	GTGGGTCTGG	GACCTCTTAC	TCTCTCACAA	TCAGCAGAGT	GGAGGCTGAA	240
GATGCTGCCA	CTTATTACTG	CCAGCAGTGG	AGTATTAACC	CACGGACGTT	CGGTGGAGGC	300
ACCAAGCTGG	AAATCAAACG	G				321

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu 1 5 15 10 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr 25 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 40 Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe 55 60 Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn 70 75 Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys 90 Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly 105 Gln Gly Thr Leu Val Thr Val Ser Ala 115 120

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn Tyr Gly Met Asn

1

5

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys

1

5

10

15

Gly

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr

1 5 10

- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

35 40 45

- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Ala Ser Ser Ser Val Asn Tyr Met His

1 5 10

- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Thr Ser Asn Leu Ala Ser
1 5

- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gln Gln Trp Ser Ile Asn Pro Arg Thr

- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAACTAGTGC AATCTGGGTC TGAGTTGAAG AAGCCTGGGG CCTCAGTGAA GGTTTCCTGC
AAGGCCTCTG GATACACCTT CACTAACTAT GGAATGAACT GGGT

(A) LENGTH: 108 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
	60
TTGAAGTCAT CAACATATGT TGACTTTCCA TTTCTGGTGT TTATCCATCC CATCCACTCG	108
AGCCCTTGTC CAGGGGCCTG TCGCACCCAG TTCATTCCAT AGTTAGTG	100
(2) INFORMATION FOR SEQ ID NO:17:	
(2) INFORMATION FOR SEQ 12 10012	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 107 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GTCAACATAT GTTGATGACT TCAAGGGGCG GTTTGTCTTC CCTCTGTCAG CACGGCATAT	60
	107
CTACAGATCA GCAGCCTAAA GGCTGACGAC ACTGCAGTGT ATTACTG	±07

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 91 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
GGTACCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGCACA	60
GTAATACACT GCAGTGTCGT CAGCCTTTAG G	91
(2) INFORMATION FOR SEQ ID NO:19:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 337 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(ix) FEATURE:	

(B) LOCATION: 2...337

(A) NAME/KEY: Coding Sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

															G AAG	49
	eu va L	31 GJ	III Se	5r G1		er Gi	u be	։ս ոչ	,s L) 1(.0 01	.у Ал	.a be	15		
										ACT						97
Val	Ser	Cys	Lys 20	Ala	Ser	Gly	Tyr	Thr 25	Phe	Thr	Asn	Tyr	Gly 30	Met	Asn	
										GAG						145
Trp	Val	Arg 35	Gln	Ala	Pro	Gly	Gln 40	Gly	Leu	Glu	Trp	Met 45	Gly	Trp	Ile	
										GAT Asp						193
ASII	50	Arg	ASII	CLY	1 95	55		-2-	741	1100	60		-1~	1	5	
										ACG Thr						241
65	vai	rne	per	пец	70	1111	DCI	vai	DCI	75	2114	- 7 -	Lea	0211	80	
										TAT						289
Ser	Ser	Leu	Lys	A1a 85	Asp	Asp	Thr	Ala	90	Tyr	Tyr	Cys	Ala	95	GIU	
										TAC						33"
Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe 105	Thr	Tyr	Trp	Gly	Gln 110	Gly	Thr	

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala Ser Val Lys 5 10 Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn 25 20 Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile 40 Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg 55 60 Phe Val Phe Ser Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile 70 75 Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu 95 85 90

- Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr 100 105 110
 - (2) INFORMATION FOR SEQ ID NO:21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE:
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCTACTAGTG CAATCTGGGT CTGAGTTGAA GCC

- (2) INFORMATION FOR SEQ ID NO:22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs

- (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22: TGGGTACCCT GGCCCCAGTA AGTAAAAGGG 30 (2) INFORMATION FOR SEQ ID NO:23: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 97 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (ix) FEATURE: (A) NAME/KEY: Coding Sequence (B) LOCATION: 27...95 (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 53

Met Gly Trp Ser Cys Ile Ile Leu Phe

1 5

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG GTC CAA CTA GT
Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu

10 20

97

- (2) INFORMATION FOR SEQ ID NO:24:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Gln Val Gln Leu
20

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE:
 - (vi) ORIGINAL SOURCE:

TCTTCTTGGT AGCAACAGCT ACAGGTGTCC ACTCCCAGGT CCAACTGCAG	110
2) INFORMATION FOR SEQ ID NO:26:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
GGAGACGCCA TCGAATTCTG A	21
(2) INFORMATION FOR SEQ ID NO:27:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 30 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
GATTGCACTA GTTGGACCTG GGAGTGGACA	30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGACGCCA TCGAATTCTG AGCACACAGG ACCTCACCAT GGGATGGAGC TGTATCATCC

TCTGCGACCC ACT

(2) INFORMATION FOR SEQ ID NO:28:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 77 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
CTAGAGTGGG TCGCAGAGAT CTCTGATGGT GGTAGTTACA CCTACTATCC AGACACTGTG ACGGGCCGGT TCACGAT	60 77
(2) INFORMATION FOR SEQ ID NO:29:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 73 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
ATCGTGAACC GGCCCGTCAC AGTGTCTGGA TAGTAGGTGT AACTACCACC ATCAGAGATC	60

65

(2) INFORMATION FOR SEQ ID NO:30:

(i)	SEOUENCE	CHARACTERISTICS:
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- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...363

70

(D) OTHER INFORMATION: F9HZHC 1-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAG	GTG	CAA	CTA	GTG	CAA	TCT	GGG	TCT	GAG	TTG	AAG	AAG	CCT	GGG	GCC	4
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala	
1				5					10					15		
TCA	GTG	AAG	\mathtt{GTT}	TCC	TGC	AAG	GCC	TCT	GGA	TAC	ACC	TTC	ACT	AAC	TAT	9
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	
			20					25					30			
GGA	ATG	AAC	TGG	GTG	CGA	CAG	GCC	CCT	GGA	CAA	GGG	CTC	GAG	TGG	ATG	14
Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35					40					45				
GGA	TGG	ATA	AAC	ACC	AGA	AAT	GGA	AAG	TCA	ACA	TAT	GTT	GAT	GAC	TTC	19
G1y	Trp	Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	
	50					55					60					
AAG	GGA	CGG	TTT	GTC	TTC	TCC	TTG	GAC	ACC	TCT	GTC	AGC	ACG	GCA	TAT	24
Lys	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr	

75

CTA	CAG	ATC	AGC	AGC	CTA	AAG	GCT	GAC	GAC	ACT	GCA	GTG	TAT	TAC	TGT	288
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
GCG	AGA	GAA	GGG	AAT	ATG	GAT	GGT	TAC	TTC	CCT	TTT	ACT	TAC	TGG	GGC	336
Ala	Arg	Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	
			100					105					110			
CAG	GGT	ACC	CTG	GTC	ACC	GTC	TCC	TCA								363
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		115					120									

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20					25					30		
Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			
Gly	Trp	Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe
	50					55					60				
Lys	Gly	Arg	Phe	Val	Phe	Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr
65					70					75					80
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly
			100					105					110		

Gln Gly Thr Leu Val Thr Val Ser Ser

115	120				
(2) INFORMATION	ON FOR SEQ ID NO:32:				
(i) SE	QUENCE CHARACTERISTI	CS:			
(A)	LENGTH: 165 base pai	rs			
(B)	TYPE: nucleic acid				
(C)	STRANDEDNESS: single	!			
(D) '	TOPOLOGY: linear				
(ii) M	OLECULE TYPE: cDNA				
(iii)	HYPOTHETICAL: NO				
(iv) A	NTISENSE: NO				
	AGMENT TYPE:				
(vi) 0	RIGINAL SOURCE:				
(xi) S	EQUENCE DESCRIPTION:	SEQ ID NO:	32:		
AGTACTGACA C	AGTCTCCAG CCACCCTGTC	TTTGTCTCCA	GGGGAAAGAG	CCACCCTCTC	60
CTGCAGGGCC A	GCTCAAGTG TAAATTACAT	' GCACTGGTAC	CAACAGAGAC	CTGGCCAGGC	120
TCCCAGGCTC C	TCATCTATG CCACTAGTAA	CCTGGCTTCT	GGCAT		165
(2) INFORMATION	ON FOR SEQ ID NO:33:				
(i) SE	QUENCE CHARACTERISTI	CS:			
(A)	LENGTH: 146 base pai	rs			
(B)	TYPE: nucleic acid				
	STRANDEDNESS: single	2			
(D)	TOPOLOGY: linear				
(ii) M	OLECULE TYPE: cDNA				
(iii)	HYPOTHETICAL: NO				
(iv) A	NTISENSE: NO				
(v) FR	AGMENT TYPE:				
(vi) 0	RIGINAL SOURCE:				
(xi) S	EQUENCE DESCRIPTION:	SEQ ID NO:	33:		
CCGCGGGTTA A	TACTCCACT GCTGACAGTA	ATAAACCGCA	AAATCTTCAG	GCTCTAGACT	60
GCTGATGGTG A	GAGTGAAAT CTGTCCCAGA	CCCGGATCCA	CTGAACCTGG	CTGGGATGCC	120

146

AGAAGCCAGG TTACTAGTGG CATAGA

(2) INFORMATION FOR SEQ ID NO:34:

(i)	SEQUENCE	CHARACTERISTICS:
-----	----------	------------------

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 2...280
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

- A GTA CTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG GAA AGA

 Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly Glu Arg

 1 5 10 15
- GCC ACC CTC TCC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG 97

 Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met His Trp

 20 25 30
- TAC CAA CAG AGA CCT GGC CAG GCT CCC AGG CTC CTC ATC TAT GCC ACT

 Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Thr

 35

 40

 45
- AGT AAC CTG GCT TCT GGC ATC CCA GCC AGG TTC AGT GGA TCC GGG TCT 193

 Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser

 50 55 60
- GGG ACA GAT TTC ACT CTC ACC ATC AGC AGT CTA GAG CCT GAA GAT TTT 241
 Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe
 70 75 80

82

- C - P - 2

GCG GTT TAT TAC TGT CAG CAG TGG AGT ATT AAC CCG CGG
Ala Val Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg
85 90

280

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

- (2) INFORMATION FOR SEQ ID NO:36:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
TCGAGTACTG ACACAGTCTC CAGCCAC	27
(2) INFORMATION FOR SEQ ID NO:37:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 27 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
GACCGCGGGT TAATACTCCA CTGCTGA	27
(2) INFORMATION FOR SEQ ID NO:38:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 94 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	

(ix) FEATURE:

(A)	NAME/KEY:	Coding	Sequence
(B)	LOCATION:	2792	2

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 53

Met Gly Trp Ser Cys Ile Ile Leu Phe

1 5

94

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC GAG ATA GTA CT
Leu Val Ala Thr Ala Thr Gly Val His Ser Glu Ile Val

10 20

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly

1 5 10 15

Val His Ser Glu Ile Val

- (2) INFORMATION FOR SEQ ID NO:40:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
GACTGTGTCA GTACTATCTC GGAGTGGACA 30
(2) INFORMATION FOR SEQ ID NO:41:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
GGGCAGCCTC CTAAGTTGCT CATTTACTGG GCGTCGACTA GGGAATCTGG GGTAC 55
(2) INFORMATION FOR SEQ ID NO:42:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCC	AGAT'	rcc (C'TAG'	rcga(CG CC	CCAG	raaa:	r gag	GCAA	CTTA	GGA	GGCT	GCC (C		5	1
(2)	ENFO	RMAT	ION I	FOR S	SEQ I	ID N	0:43	:									
	(:	i) SI	EQUEI	NCE (CHAR!	ACTEI	RIST	ICS:									
		(A)	LENG	GTH:	321	base	e pa:	irs									
		(B)	TYPI	Ξ: nι	ıclei	ic a	cid										
		(C)	STR	ANDEI	ONESS	S: s:	ingle	е									
		(D)	TOP	OLOG	Y: 1i	inea	r										
	(:	ii) 1	MOLE	CULE	TYPI	E: cl	ONA										
	(:	iii)	HYPO	OTHE:	ricai	J: NO)										
	(:	iv) A	ITNA	SENSI	E: NO)											
	(7	J) FI	RAGMI	ENT ?	TYPE:	:											
	(7	<i>J</i> i) (ORIG:	INAL	SOU	RCE:											
	(:	ix) I	FEAT	JRE:													
		(A)	IAN (ME/KI	ΞY: (Codi	ng Se	equei	nce								
		(B)) LO	CATI	ON: 1	L:	321										
		(D)) OTI	HER .	INFO	RMAT:	ION:	F9H	ZLC1-	-0							
	(2	ki) S	SEQUI	ENCE	DESC	CRIP	rion	: SE	Q ID	NO:	43:						
C 3 3	א תויא	CMA	cmc	7 C 7	CAC	m/cm	CCA	ccc	7 CC	CITIC	TCT	mmc	mom	CCA	ccc	48	
											Ser					40	
1	116	vai	Беа	5	GIII	Set	FLO	ALA	10	пеα	Ser	пец	Set	15	GIY		
_				J					10					1.0			
GAA	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	96	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met		
			20					25					30				
CAC	TGG	TAC	CAA	CAG	AGA	CCT	GGC	CAG	GCT	CCC	AGG	CTC	CTC	ATC	TAT	144	
His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr		
		35					40					45					

GCC	ACT	AGT	AAC	CTG	GCT	TCT	GGC	ATC	CCA	GCC	AGG	TTC	AGT	GGA	TCC	192
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Ile	Pro	Ala	Arg	Phe	Ser	Gly	Ser	
	50					55					60					
GGG	TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTA	GAG	CCT	GAA	240
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	
65					70					75					80	
GAT	$\mathbf{T}\mathbf{T}\mathbf{T}$	GCG	GTT	TAT	TAC	$\mathbb{T} \mathbb{G} \mathbb{T}$	CAG	CAG	TGG	AGT	ATT	AAC	CCG	CGG	ACG	288
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr	
				85					90					95		
TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	CGA						321
Phe	Gly	Gly	Gly	Thr	Lys	Va1	Glu	Ile	Lys	Arg						
			100					105								
	-1															

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
			100					105							

- (2) INFORMATION FOR SEQ ID NO:45:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCTGGACAAG GGCTCAAGTG GATGGGATGG ATAAACACCA GAAATGGAAA GTCAACATAT 60
GTTGATGACT TCAAGGGACG GTTTGTCTTC TCTCTAGACT CCTCTGTCAG CACGGCATAT 120
CTACAGATCA GCAG 134

- (2) INFORMATION FOR SEQ ID NO:46:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

no more example to the

GGTACCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGTACA	60
GTAATACACT GCAGTGTCGT CAGCCTTTAG GCTGCTGATC TGTAGATATG CCGTGCTGAC 1	20
AGAGGAGTCT AGAG	34
(2) INFORMATION FOR SEQ ID NO:47:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 225 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(11) NOT FOUND THE TOTAL	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(ix) FEATURE:	
(2) MAMERIAN Co. Since Comment	
(A) NAME/KEY: Coding Sequence	
(B) LOCATION: 1225	
(D) OTHER INFORMATION:	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:47:	
CCT GGA CAA GGG CTC AAG TGG ATG GGA TGG ATA AAC ACC AGA AAT GGA 4	18
Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr Arg Asn Gly	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr Arg Asn Gly

1 5 10 15

AAG TCA ACA TAT GTT GAT GAC TTC AAG GGA CGG TTT GTC TTC TCT CTA

96
Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser Leu
20 25 30

GAC TCC TCT GTC AGC ACG GCA TAT CTA CAG ATC AGC AGC CTA AAG GCT

Asp Ser Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala
35 40 45

GAC GAC ACT GCA GTG TAT TAC TGT ACG AGA GAA GGG AAT ATG GAT GGT

Asp Asp Thr Ala Val Tyr Tyr Cys Thr Arg Glu Gly Asn Met Asp Gly

50 55 60

225

TAC TTC CCT TTT ACT TAC TGG GGC CAG GGT ACC

Tyr Phe Pro Phe Thr Tyr Trp Gly Gln Gly Thr

65 70 75

- (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

- (2) INFORMATION FOR SEQ ID NO:49:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
TTTCCTGGAC AAGGGCTCAA GTGGATG	27
(2) INFORMATION FOR SEQ ID NO:50:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 24 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(V) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
TTTGGTACCC TGGCCCCAGT AAGT	24
(2) INFORMATION FOR SEQ ID NO:51:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 363 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(ii) MOLECULE III. ODIA: (iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(1V) ANTISENSE: NO (V) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(AT) OUTGINING SECTION	

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...363

(D) OTHER INFORMATION: F9HZHC 1-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CAG	CTC	$C \lambda \lambda$	СТА	CTC.	$C\Delta\Delta$	ጥር ጥ	GGG	ФСФ	GAG	ጥጥር	ΔAG	ΔAG	CCT	GGG	GCC	4	8
														Gly		_	0
1	• • • •	0		5			1		10		-1 -	-1		15			
TCA	GTG	AAG	GTT	TCC	TGC	AAG	GCC	TCT	GGA	TAC	ACC	TTC	ACT	AAC	TAT	9	6
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr		
			20					25					30				
~~~			maa	~=~		~~~	~~~	~~m	223	G 7 3	222	GE G	330	maa	3 mg	2.4	4
									_		_			TGG		14	4
GTĀ	Mec	35	пр	Val	Arg	GIII	40	PIO	GIY	GIII	GIY	45	пур	Trp	Mec		
		33					10					10					
GGA	TGG	ATA	AAC	ACC	AGA	AAT	GGA	AAG	TCA	ACA	TAT	GTT	GAT	GAC	TTC	19	2
Gly	Trp	Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe		
	50					55					60						
														GCA		24	0
ьуs 65	GIY	Arg	Pne	Val	70	Ser	Leu	Asp	Ser	Ser 75	Val	Ser	Thr	Ala	TYr		
0.5					70					, ,					00		
CTA	CAG	ATC	AGC	AGC	СТА	AAG	GCT	GAC	GAC	ACT	GCA	GTG	TAT	TAC	TGT	28	8
Leu	Gln	Ile	Ser	Ser	Leu	Lys	Ala	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
				85					90					95			
														TGG _		33	6
Thr	Arg	GLu	_	Asn	Met	Asp	GLy	_	Phe	Pro	Phe	Thr	_	Trp	Gly		
			100					105					110				
CAG	GGT	ACC	CTG	GTC	ACC	GTC	TCC	TCA								3	63
	Gly																-
		115					120										

#### (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 121 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:
- Gln Val Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys Pro Gly Ala 1 5 10 15
- Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
  20 25 30
- Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Lys Trp Met
  35 40 45
- Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe
  50 55 60
- Lys Gly Arg Phe Val Phe Ser Leu Asp Ser Ser Val Ser Thr Ala Tyr
  65 70 75 80
- Leu Gln Ile Ser Ser Leu Lys Ala Asp Asp Thr Ala Val Tyr Tyr Cys
  85 90 95
- Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
  100 105 110
- Gln Gly Thr Leu Val Thr Val Ser Ser 115 120
- (2) INFORMATION FOR SEQ ID NO:53:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 82 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
CAACAGAGAC CTGGCCAGGC TCCCAAGCCC TGGATCTATG CCACGAGTAA CCTGGCTAGC	50
GGCGTCCCAG CCAGGTTCAG TG	32
(2) INFORMATION FOR SEQ ID NO:54:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 90 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:	
GATCCACTGA ACCTGGCTGG GACGCCGCTA GCCAGGTTAC TCGTGGCATA GATCCAGGGC	60
TTGGGAGCCT GGCCAGGTCT CTGTTGGTAC	90
(2) INFORMATION FOR SEQ ID NO:55:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 27 amino acids	
(B) TYPE: amino acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: peptide	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE: internal	

(vi)	ORIGINAL	SOURCE:
(xi)	SEQUENCE	DESCRIP

PTION: SEQ ID NO:55:

Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr Ala Thr Ser 5 10 Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser

- (2) INFORMATION FOR SEQ ID NO:56:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 321 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
  - (ix) FEATURE:
    - (A) NAME/KEY: Coding Sequence
    - (B) LOCATION: 1...321
    - (D) OTHER INFORMATION: F9HZLC 1-1
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
- GAA ATA GTA CTG ACA CAG TCT CCA GCC ACC CTG TCT TTG TCT CCA GGG 48 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly 1 5 10 15
- GAA AGA GCC ACC CTC TCC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG 96 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Ser Ser Val Asn Tyr Met 20 25 30
- CAC TGG TAC CAA CAG AGA CCT GGC CAG GCT CCC AAG CCC TGG ATC TAT 144 His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Lys Pro Trp Ile Tyr 35 40 45

GCC	ACG	AGT	AAC	CTG	GCT	AGC	GGC	GTC	CCA	GCC	AGG	TTC	AGT	GGA	TCC	192
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	
	50					55					60					
GGG	TCT	GGG	ACA	GAT	TTC	ACT	CTC	ACC	ATC	AGC	AGT	CTA	GAG	CCT	GAA	240
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	
65					70					75					80	
GAT	TTT	GCG	GTT	TAT	TAC	TGT	CAG	CAG	TGG	AGT	ATT	AAC	CCG	CGG	ACG	288
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr	
				85					90					95		
TTC	GGC	GGA	GGG	ACC	AAG	GTG	GAG	ATC	AAA	CGA						321
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg						
			100					105								

- (2) INFORMATION FOR SEQ ID NO:57:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 107 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE: internal
  - (vi) ORIGINAL SOURCE:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr
				85					90					95	
Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
			100	)		105									

- (2) INFORMATION FOR SEQ ID NO:58:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

(2) INFORMATION FOR SEQ ID NO:59:

# GATCCGGGTC TGGGACAGAT TACACTCTCA CGATATCCAG T

41

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CTAGACTGGA TATCGTGAGA GTGTAATCTG TCCCAGACCC G

## (2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO:61:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 321 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...321
  - (D) OTHER INFORMATION: F9HZLC 1-2

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAA	ATA	GTA	CTG	ACA	CAG	TCT	CCA	GCC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	4.8	3
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly		
1				5					10					15			
GAA	AGA	GCC	ACC	CTC	TCC	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	96	5
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met		
			20					25					30				
CAC	TGG	TAC	CAA	CAG	AGA	CCT	GGC	CAG	GCT	CCC	AAG	CCC	TGG	ATC	TAT	14	4
His	Trp	Tyr	Gln	Gln	Arg	Pro	Gly	Gln	Ala	Pro	Lys	Pro	Trp	Ile	Tyr		
		35					40					45					
			AAC													19	2
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser		
	50					55					60						
																	_
			ACA													24	0
Gly	Ser	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro			
65					70					75					80		
																	_
			GTT													28	8
Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln		Ser	Ile	Asn	Pro		Thr		
				85					90					95			
										~~~						2	21
			GGG													3	∠ ⊥
Phe	Gly	Gly	Gly		Lys	Val	Glu			Arg							
			100					105									

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

	1	(xi)	SEQU	JENCI	E DES	SCRI	10IT9	N: SI	EQ II	O NO:	:62:				
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg		Ser	Ser	Ser	Val		Tyr	Met
			20					25					30		
His	Trp		Gln	Gln	Arg	Pro		Gln	Ala	Pro	Lys		Trp	lle	ТУr
		35					40		_		_	45	a	G3	G
Ala		Ser	Asn	Leu	Ala		Giy	Val	Pro	Ата	Arg 60	Pne	ser	GTĀ	ser
a 1	50	a 1	m1	7		55	Т он	шЬ∽	т10	Sor		T.011	Glu	Pro	Glu
	Ser	GTĀ	Thr	Asp	70	TILL	ьеи	1111	TTE	75	Ser	пеа	Oiu	110	80
65 750	Dhe	Δla	Val	Туг		Cvs	Gln	Gln	Trp		Ile	Asn	Pro	Arq	Thr
ASP	1116	ALG	Val	85	-1-	0,10	0		90					95	
Phe	Glv	Glv	Gly		Lys	Val	Glu	Ile	Lys	Arg					
	1	1	100		-			105	_						
(2)	INF	(i) (A (B (C	TION SEQU) LE) TY) ST) TO	ENCE NGTH PE: RAND	CHA : 16 nucl EDNE	RACT 5 ba eic SS:	ERIS se p acid sing	TICS airs	:						
		(iii (iv) (v) (vi)	MOL) HY ANT FRAG ORI	POTH ISEN MENT	ETIC ISE: TYP L SC	AL: NO E: URCE	NO		SEO I	D NC) • 63 •				
7 . C	·መአ <i>ር</i> ጣ	(XI)											'AGAG	: TGA	CCATCAC

CTGCAGGGCC AGCTCAAGTG TAAATTACAT GCACTGGTAC CAGCAGAAGC CAGGTAAGGC

TCCAAAGCCT TGGATCTACG CCACTAGTAA CCTGGCTTCT GGTGT

(2) INFORMATION FOR SEQ ID NO:64:

•	(1)	SECUENCE	CHARACTERISTICS:	
ı	1 1	OUGULE	CHANACIENISIICS.	

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CCGCGGGTTA ATACTCCACT GCTGGCAGTA GTAGGTGGCG ATATCCTCTG GCTGGAGGCT 60
GCTGATGGTG AAGGTGTAGT CTGTACCGCT ACCGGATCCG CTGAATCTGC TTGGCACACC 120
AGAAGCCAGG TTACTAGTGG CGTAGATCCA AGGCTTTGGA G 161

- (2) INFORMATION FOR SEQ ID NO:65:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 280 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE:
 - (vi) ORIGINAL SOURCE:
 - (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 2...280
 - (D) OTHER INFORMATION:

A GTA CTC ACC CAG AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA 49 Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg 5 10 15 1 GTG ACC ATC ACC TGC AGG GCC AGC TCA AGT GTA AAT TAC ATG CAC TGG 97 Val Thr Ile Thr Cys Arq Ala Ser Ser Ser Val Asn Tyr Met His Trp 20 25 30 TAC CAG CAG AAG CCA GGT AAG GCT CCA AAG CCT TGG ATC TAC GCC ACT 145 Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr Ala Thr 35 40 45 AGT AAC CTG GCT TCT GGT GTG CCA AGC AGA TTC AGC GGA TCC GGT AGC 193 Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser 50 55 GGT ACA GAC TAC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAT ATC 241 Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile 75 65 70 80

90

280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

(2) INFORMATION FOR SEQ ID NO:66:

85

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids

GCC ACC TAC TGC CAG CAG TGG AGT ATT AAC CCG CGG

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

- (2) INFORMATION FOR SEO ID NO:67:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TTTAGTACTC ACCCAGAGCC CAAGCAG

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68: 27 TTCCGCGGGT TAATACTCCA CTGCTGG (2) INFORMATION FOR SEQ ID NO:69: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69: 33 CTCGAGCAGT ACTATCTGGG AGTGGACACC TGT (2) INFORMATION FOR SEQ ID NO:70:
- - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE: N-terminal
 - (vi) ORIGINAL SOURCE:

	(xi)	SEOUENCE	DESCRIPTION:	SEO	ID	NO:70
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Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala 1 5 10 15 Ala

- (2) INFORMATION FOR SEQ ID NO:71:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE:
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGGAC TGTGGCGG

48

- (2) INFORMATION FOR SEQ ID NO:72:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CGCCGCCACA GTCCGTTTGA TTTCCACCTT GGTCCCTTGG CCGAACGTCC GC

(2) INFORMATION FOR SEQ ID NO:73:

131	CECTIENCE	CHARACTERISTICS:
(1)	SECUENCE	CHARACIERISITCS.

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...321
 - (D) OTHER INFORMATION: F9HZLC 2-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAG	ATA	GTA	CTC	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	AGC	GTG	GGT	48
Gln	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
GAC	AGA	GTG	ACC	ATC	ACC	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	
			20					25					30			
CAC	TGG	TAC	CAG	CAG	AAG	CCA	GGT	AAG	GCT	CCA	AAG	CCT	TGG	ATC	TAC	144
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	
		35					40					45				
GCC	ACT	AGT	AAC	CTG	GCT	TCT	GGT	GTG	CCA	AGC	AGA	TTC	AGC	GGA	TCC	192
Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser	
	50					55					60					
GGT	AGC	GGT	ACA	GAC	TAC	ACC	TTC	ACC	ATC	AGC	AGC	CTC	CAG	CCA	GAG	240
															Glu	
65		4		-	70					75					80	
7.5																

GAT ATC GCC ACC TAC TAC TGC CAG CAG TGG AGT ATT AAC CCG CGG ACG 288

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr

85 90 95

TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA CGG
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

321

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 5 10 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met 20 25 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Trp Ile Tyr 35 40 45 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 55 Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu 70 75 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr 85 90 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg 100 105

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 27...94
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 53

Met Gly Trp Ser Cys Ile Ile Leu Phe

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94

TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CT
Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu
10 20

- (2) INFORMATION FOR SEQ ID NO:76:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

(v) FRAGMENT TYPE: internal

	(vi) ORIGINAL SOURCE:
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:
	Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15 Val His Ser Gln Ile Val Leu 20
	(2) INFORMATION FOR SEQ ID NO:77:
all datal tatal at the case when	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 401 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (ix) FEATURE: (A) NAME/KEY: Coding Sequence (B) LOCATION: 27401 (C) OTHER INFORMATION: F9HZLC 1-3
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:
	GAATTCTGAG CACACAGGAC CTCACC ATG GGA TGG AGC TGT ATC ATC CTC TTC 53 Met Gly Trp Ser Cys Ile Ile Leu Phe 1 5
	TTG GTA GCA ACA GCT ACA GGT GTC CAC TCC CAG ATA GTA CTG ACA CAG Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Ile Val Leu Thr Gln 10 25

TCT	CCA	GCC	ACC	CTG	TCT	TTG	TCT	CCA	GGG	GAA	AGA	GCC	ACC	CTC	TCC	149
Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	
				30					35					40		
TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	CAC	TGG	TAC	CAA	CAG	AGA	197
Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	His	Trp	Tyr	Gln	Gln	Arg	
			45					50					55			
CCT	GGC	CAG	GCT	CCC	AAG	CCC	TGG	ATC	TAT	GCC	ACG	AGT	AAC	CTG	GCT	245
Pro	Gly	Gln	Ala	Pro	Lys	Pro	Trp	Ile	Tyr	Ala	Thr	Ser	Asn	Leu	Ala	
		60					65					70				
AGC	GGC	GTC	CCA	GCC	AGG	TTC	AGT	GGA	TCC	GGG	TCT	GGG	ACA	GAT	TAC	293
Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	
	75					80					85					
ACT	CTC	ACG	ATA	TCC	AGT	CTA	GAG	CCT	GAA	GAT	TTT	GCG	GTT	TAT	TAC	341
Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	
90					95					100					105	
TGT	CAG	CAG	TGG	AGT	ATT	AAC	CCG	CGG	ACG	TTC	GGC	GGA	GGG	ACC	AAG	389
Cys	Gln	Gln	Trp	Ser	Ile	Asn	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
-				110					115					120		
GTG	GAG	ATC	AAA													401
Val	Glu	Ile	Lys													
			125													

- (2) INFORMATION FOR SEQ ID NO:78:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:

	(>	ki) S	SEQUE	ENCE	DESC	RIPT	CION:	SEÇ) ID	NO:	78:				
Met 1	Gly	Trp	Ser	Cys 5	Ile	Ile	Leu	Phe	Leu 10	Val	Ala	Thr	Ala	Thr 15	Gly
Val	His	Ser	Gln 20	Ile	Val	Leu	Thr	Gln 25	Ser	Pro	Ala	Thr	Leu 30	Ser	Leu
Ser	Pro	Gly 35	Glu	Arg	Ala	Thr	Leu 40	Ser	Cys	Arg	Ala	Ser 45	Ser	Ser	Val
Asn	Tyr 50	Met	His	Trp	Tyr	Gln 55	Gln	Arg	Pro	Gly	Gln 60	Ala	Pro	Lys	Pro
Trp 65	Ile	Tyr	Ala	Thr	Ser 70	Asn	Leu	Ala	Ser	Gly 75	Val	Pro	Ala	Arg	Phe 80
Ser	Gly	Ser	Gly	Ser 85	Gly	Thr	Asp	Tyr	Thr	Leu	Thr	Ile	Ser	Ser 95	Leu
Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr 105	Cys	Gln	Gln	Trp	Ser 110	Ile	Asn
Pro	Arg	Thr 115	Phe	Gly	Gly	Gly	Thr 120	Lys	Val	Glu	Ile	Lys 125			
(2)	INFO	RMAT	ION :	FOR	SEQ	ID N	0:79	:							

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

AGGCCTCTGG ATACACCTTC ACTAACTATG GAATGAACTG GGTGCGACAG GCCCCTGGAC

AAGGGCTCGA GTGGATGGGA T

- (2) INFORMATION FOR SEQ ID NO:80:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
TGTCTAGAGA GAAGACAAAC CGTCCCTTGA AGTCATCAAC ATATGTTGAC TTTCCATTTC	60
TGGTGTTTAT CCATCCCATC CACTCGAGCC CTTGTCCAG	99
(2) INFORMATION FOR CEO ID NO. 91.	
(2) INFORMATION FOR SEQ ID NO:81:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 87 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
GGTTTGTCTT CTCTCTAGAC ACCTCTGTCA GCACGGCATA TCTACAGATC AGCAGCCTAA	60
AGGCTGAGGA CACTGCAGTG TATTTCT	87
(2) INFORMATION FOR SEQ ID NO:82:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 86 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
GGTACCCTGG CCCCAGTAAG TAAAAGGGAA GTAACCATCC ATATTCCCTT CTCTCGTACA	60
GAAATACACT GCAGTGTCCT CAGCCT	86
(2) INFORMATION FOR SEQ ID NO:83:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 278 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
ALL MOT DOWN B. EVENT TOWN	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(ix) FEATURE:	
(A) NAME/KEY: Coding Sequence	
(B) LOCATION: 3278	
(D) OTHER INFORMATION:	
\- /	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
AG GCC TCT GGA TAC ACC TTC ACT AAC TAT GGA ATG AAC TGG GTG CGA	47
Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg	
1 5 10 15	
CAG GCC CCT GGA CAA GGG CTC GAG TGG ATG GGA TGG ATA AAC ACC AGA	95
Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Arg	
20 25 30	

AAT	GGA	AAG	TCA	ACA	TAT	GTT	GAT	GAC	TTC	AAG	GGA	CGG	TTT	GTC	TTC	143
Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	Lys	Gly	Arg	Phe	Val	Phe	
			35					40					45			
TCT	CTA	GAC	ACC	\mathtt{TCT}	GTC	AGC	ACG	GCA	TAT	CTA	CAG	ATC	AGC	AGC	CTA	191
Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Ser	Ser	Leu	
		50					55					60				
AAG	GCT	GAG	GAC	ACT	GCA	GTG	TAT	TTC	TGT	ACG	AGA	GAA	GGG	AAT	ATG	239
Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys	Thr	Arg	Glu	Gly	Asn	Met	
	65					70					75					
GAT	GGT	TAC	TTC	CCT	TTT	ACT	TAC	TGG	GGC	CAG	GGT	ACC				278
Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	Gln	Gly	Thr				
80					85					90						

- (2) INFORMATION FOR SEQ ID NO:84:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE: internal
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn Trp Val Arg Gln 10 1 Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Arg Asn 25 Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys Gly Arg Phe Val Phe Ser 40 Leu Asp Thr Ser Val Ser Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys 50 55 60 Ala Glu Asp Thr Ala Val Tyr Phe Cys Thr Arg Glu Gly Asn Met Asp 75 80 65 70

Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	Gln	Gly	Thi
				85					90		

- (2) INFORMATION FOR SEQ ID NO:85:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE:
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

AGGCCTCTGG ATACACCTTC ACTAACTATG

30

- (2) INFORMATION FOR SEQ ID NO:86:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GGTACCCTGG CCCCAGTAAG TAAAAG

- (2) INFORMATION FOR SEQ ID NO:87:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCAGACTCGA CTAGTTGGAT CTGGGAGTGG ACACCTG

- (2) INFORMATION FOR SEQ ID NO:88:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 446 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 27...446
 - (D) OTHER INFORMATION: F9HZHC 3-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAAT	TCTO	GAG C	CACAC	CAGGA	AC CI	CACC									TTC Phe	53
							1				5					
TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC	TCC	CAG	ATC	CAA	CTA	GTG	CAA	101
Leu	Val	Ala	Thr	Ala	Thr	Gly	Val	His	Ser	Gln	Ile	Gln	Leu	Val	Gln	
10					15					20					25	
TCT	GGG	TCT	GAG	TTG	AAG	AAG	CCT	GGG	GCC	TCA	GTG	AAG	GTT	TCC	TGC	149
Ser	Gly	Ser	Glu	Leu	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	
				30					35					40		
AAG	GCC	TCT	GGA	TAC	ACC	TTC	ACT	AAC	TAT	GGA	ATG	AAC	TGG	GTG	CGA	197
Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Arg	
			45					50					55			
CAG	GCC	CCT	GGA	CAA	GGG	CTC	GAG	TGG	ATG	GGA	TGG	ATA	AAC	ACC	AGA	245
Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Arg	
		60					65					70				
AAT	GGA	AAG	TCA	ACA	TAT	GTT	GAT	GAC	TTC	AAG	GGA	CGG	TTT	GTC	TTC	293
Asn	_	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	Lys		Arg	Phe	Val	Phe	
	75					80					85					
TCT	CTA	GAC	ACC	TCT	GTC	AGC	ACG	GCA	TAT	CTA	CAG	ATC	AGC	AGC	CTA	341
Ser	Leu	Asp	Thr	Ser	Val	Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Ser	Ser		
90					95					100					105	
AAG	GCT	GAG	GAC	ACT	GCA	GTG	TAT	TTC	TGT	ACG	AGA	GAA	GGG	AAT	ATG	389
Lys	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys	Thr	Arg	Glu	Gly	Asn	Met	
				110					115					120		
GAT	GGT	TAC	TTC	CCT	TTT	ACT	TAC	TGG	GGC	CAG	GGT	ACC	CTG	GTC	ACC	437
Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	
			125					130					135			
GTC	TCC	TCT														446
Val	Ser	Ser														
		140														

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 140 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Gln Ile Gln Leu Val Gln Ser Gly Ser Glu Leu Lys Lys 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45

Thr Asn Tyr Gly Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 50 55 60

Glu Trp Met Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val 65 70 75 80

Asp Asp Phe Lys Gly Arg Phe Val Phe Ser Leu Asp Thr Ser Val Ser 85 90 95

Thr Ala Tyr Leu Gln Ile Ser Ser Leu Lys Ala Glu Asp Thr Ala Val

Tyr Phe Cys Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr
115 120 125

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser 130 135 140

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO

(1V) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
AGTACTGACA CAGTCTCCAT CCTCCCTGTC TGCATCTGTT GGGGACAGAG TCACCATCAC	60
TTGCAGGGCC AGCTCAAGTG TAAATTACAT	90
(2) INFORMATION FOR SEQ ID NO:91:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 108 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(2) 10102011 2111011	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(12)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
CTTGATGGGA CGCCGCTAGC CAGGTTACTC GTGGCATAGA TCCAGGGCTT GGGAGCTTTG	60
CCAGGTTTCT GTTGGTACCA GTGCATGTAA TTTACACTTG AGCTGGCC	108
(2) INFORMATION FOR SEQ ID NO:92:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 108 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
• • • • • • • • • • • • • • • • • • • •	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
TAACCTGGCT AGCGGCGTCC CATCAAGGTT CAGTGGATCC GGGTCTGGGA CAGATTACAC	60
TCTCACGATA TCCAGTCTAC AACCTGAAGA TTTTGCGACT TATTACTG	108
(2) INFORMATION FOR SEQ ID NO:93:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 102 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
GGCGCCGCCA CAGTTCGTTT GATCTCCAGC TTGGTCCCTC CGCCGAACGT CCGCGGGTTA	60
ATACTCCACT GCTGACAGTA ATAAGTCGCA AAATCTTCAG GT	102
(2) INFORMATION FOR SEQ ID NO:94:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 330 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A)	NAME/KEY	: Coding	Sequence

- (B) LOCATION: 2...328
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CA CAG TCT CC nr Gln Ser Pro 5			9
ACT TGC AGG (Thr Cys Arg 2			7
AAA CCT GGC A			5
GCT AGC GGC GALA Ser Gly	Arg Phe S		3
TAC ACT CTC. Tyr Thr Leu 70			1
TAC TGT CAG Tyr Cys Gln 85			9
AAG CTG GAG Lys Leu Glu 100		3:	30

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser 50 55 60

Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe 65 70 75 80

Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly 85 90 95

Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala 100 105

- (2) INFORMATION FOR SEQ ID NO:96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTISENSE: NO
 - (v) FRAGMENT TYPE:
 - (vi) ORIGINAL SOURCE:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CAAGTACTGA CACAGTCTCC ATCCTC

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

AGGGCGCCGC CACAGTTCGT TTGATC

- (2) INFORMATION FOR SEQ ID NO:98:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 412 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 27...412
 - (D) OTHER INFORMATION: F9HZLC 3-0

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAAT	TTCTO	BAG (CACAC	CAGGA	C CI	CACC					TTC Phe	53
								CAG Gln 20				101
								GAC Asp				149
								CAC His				197
								GCC Ala				245
								GGG Gly				293
								GAT Asp 100				341
								TTC Phe				389
			AAA Lys									412

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 5 10 Val His Ser Gln Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala 20 25 30 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Ser Val 40 Asn Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro 50 55 60 Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe 70 75 Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu 85 90 Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val 120 125 Va1

- (2) INFORMATION FOR SEQ ID NO:100:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
CAAATAGTAC TCTCCCAGTC TCCAGC	26
(2) INFORMATION FOR SEQ ID NO:101:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 41 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(iii) HYPOTHETICAL: NO	
(iv) ANTISENSE: NO	
(v) FRAGMENT TYPE:	
(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:	
GGATAAGCTT GGCGCCGCAA CAGTCGGTTT GATTTCCAGC T	41
(2) INFORMATION FOR SEQ ID NO:102:	
(i) SEQUENCE CHARACTERISTICS:	

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...335
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CAG	АТА	GTA	CTC	TCC	CAG	TCT	CCA	GCA	ATC	CTG	TCT	GCA	TCT	CCA	GGG	48
Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Ala	Ser	Pro	Gly	
1				5					10					15		
_				-												
GAG	AAG	GTC	ACA	ATG	ACT	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	96
Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	
	2		20					25					30			
CAC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	TCC	TCC	CCC	AAA	CCC	TGG	ATT	TAT	144
His	Trp	Tvr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr	
		35			_		40					45				
GCC	ACA	TCC	AAC	CTG	GCT	TCT	GGA	GTC	CCT	GCT	CGC	TTC	AGT	GGC	AGT	192
					Ala											
	50					55					60					
	30															
GGG	тст	GGG	ACC	TCT	TAC	TCT	CTC	ACA	ATC	AGC	AGA	GTG	GAG	GCT	GAA	240
					Tyr											
65		2			70					75					80	
0.5					, 0											
GAT	GCT	GCC	ACT	TAT	TAC	TGC	CAG	CAG	TGG	AGT	ATT	AAC	CCA	CGG	ACG	288
					Tyr											
				85	-	-			90					95		
				~ ~												
ጥጥር	GGT	GGA	GGC	ACC	AAG	CTG	GAA	ATC	AAA	CGG	ACT	GTT	GCG	GCG	CC	335
					Lys											
FIIC	дтў	GTĀ	100		د برب		0	105		3		/	110			
			T00					100								

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly 10 Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met 25 His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr 45 40 Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser 60 55 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu 75 70 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr 90 85 Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro 110 100 105

- (2) INFORMATION FOR SEQ ID NO:104:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...318

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

					CAG											48
Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	Leu	Ser	Ala	Ser	Pro	Gly	
1				5					10					15		
GAG	AAG	GTC	ACA	ATG	ACT	TGC	AGG	GCC	AGC	TCA	AGT	GTA	AAT	TAC	ATG	96
Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Asn	Tyr	Met	
			20					25					30			
					AAG											144
His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys		Trp	Ile	Tyr	
		35					40					45				
														~~~	3.00	100
					GCT											192
Ala		Ser	Asn	Leu	Ala		Gly	Val	Pro	Ala		Phe	Ser	GIY	Ser	
	50					55					60					
							om a	202	7 m.c	7.00	7 C 7	ama	CAC	CCM	CAA	240
					TAC											240
	Ser	GLY	Thr	Ser	Tyr	ser	ьeu	THE	тте	5er 75	Arg	Val	GIU	ALA	80	
65					70					13					80	
C A III	CCT	aaa	3 Cm	m z m	TAC	mcc.	CAC	CAG	ጥሮር	አርጥ	<b>አ</b> ጥጥ	AAC	CCA	CGG	ACG	288
					Tyr											200
ASD	Ala	Ата	1111	85	тАт	Cys	GIII	GIII	90	per	110	ASII	110	95	1111	
				رن					<i>J</i> 0					, ,		
ውጥር	GGT	GGA	GGC	ACC	AAG	CTG	GAA	ATC	AAA							318
					Lys											
	- <u>-</u> 1	1	100		-1-			105	<b>-</b>							

## (2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

105

- (2) INFORMATION FOR SEQ ID NO:106:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO

100

- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGATCCAAC TAGTGCAGTC TGGACCTGAG

#### (2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

### TTAAGCTTGC TAGCTGCAGA GACAGTGACC AG

- (2) INFORMATION FOR SEQ ID NO:108:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...369
  - (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

					CAG											48
Gln	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro	Gly	Glu	
1				5					10					15		
ACA	GTC	AAG	ATC	TCC	TGC	AAG	GCT	TCT	GGG	TAC	ACC	TTC	ACA	AAC	TAT	96
Thr	Val	Lys	I1e	Ser	Cys	Lys	Ala	Ser	Gly	$\operatorname{Tyr}$	Thr	Phe	Thr	Asn	Tyr	
			20					25					30			
GGA	ATG	AAC	TGG	GTG	AAG	CAG	GCT	CCA	GGA	AAG	GGT	TTA	AAG	TGG	ATG	144
Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp	Met	
		35					40					45				
GGC	TGG	ATA	AAC	ACC	AGA	AAT	GGA	AAG	TCA	ACA	TAT	GTT	GAT	GAC	TTC	192
Gly	Trp	Ile	Asn	Thr	Arg	Asn	Gly	Lys	Ser	Thr	Tyr	Val	Asp	Asp	Phe	
	50					55					60					
AAG	GGA	CGG	TTT	GCC	TTC	TCT	TTG	GAA	AGC	TCT	GCC	AGC	ACT	GCC	AAT	240
Lys	Gly	Arg	Phe	Ala	Phe	Ser	Leu	Glu	Ser	Ser	Ala	Ser	Thr	Ala	Asn	
65					70					75					80	
TTG	CAG	ATC	GAC	AAC	CTC	AAA	GAT	GAG	GAC	ACG	GCT	ACA	TAT	TTC	TGT	288
Leu	Gln	Ile	Asp	Asn	Leu	Lys	Asp	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	
			_	85					90					95		
ACA	AGA	GAA	GGG	AAT	ATG	GAT	GGT	TAC	TTC	CCT	TTT	ACT	TAC	TGG	GGC	336
Thr	Arg	Glu	Gly	Asn	Met	Asp	Gly	Tyr	Phe	Pro	Phe	Thr	Tyr	Trp	Gly	
	_		100					105					110			
CAA	GGG	ACT	CTG	GTC	ACT	GTC	TCT	GCA	GCT	AGC						369
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ala	Ser						

## (2) INFORMATION FOR SEQ ID NO:109:

120

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 123 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:
- Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu

  1 5 10 15

  Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
  20 25 30
- Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 35 40 45
- Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe
  50 55 60
- Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn 65 70 75 80
- Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys 85 90 95
- Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
  100 105 110
- Gln Gly Thr Leu Val Thr Val Ser Ala Ala Ser 115 120
  - (2) INFORMATION FOR SEQ ID NO:110:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 363 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
  - (ix) FEATURE:
    - (A) NAME/KEY: Coding Sequence
    - (B) LOCATION: 1...363

## (D) OTHER INFORMATION:

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

							~~~	0.0T	03.0	ama.	220	7 7 C	CCT	CCA	CAC	48
					CAG											4 0
	Ile	GIn	Leu	Val 5	Gln	ser	GTA	Pro	10	ьеи	пур	пур	FIU	15	Giu	
1				5					10							
ACA	GTC	AAG	ATC	TCC	TGC	AAG	GCT	TCT	GGG	TAC	ACC	TTC	ACA	AAC	TAT	96
					Cys											
		-	20		_			25					30			
GGA	ATG	AAC	TGG	GTG	AAG	CAG	GCT	CCA	GGA	AAG	GGT	TTA	AAG	TGG	ATG	144
Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Lys	Trp	Met	
		35					40					45				
																100
					AGA											192
Gly		Ile	Asn	Thr	Arg		Gly	Lys	Ser	Thr		Val	Asp	Asp	Pne	
	50					55					60					
3 3 C	CCA	ccc	արդուր	ccc	TTC	ሞርጥ	ጥጥር	GAA	AGC	тст	GCC	AGC	ACT	GCC	AAT	240
					Phe											
65	017	1129	1110		70					75					80	
TTG	CAG	ATC	GAC	AAC	CTC	AAA	GAT	GAG	GAC	ACG	GCT	ACA	TAT	TTC	TGT	288
Leu	Gln	Ile	Asp	Asn	Leu	Lys	Asp	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	
				85					90					95		
															GGC	336
Thr	Arg	Glu			. Met	Asp	Gly			Pro	Phe	Thr			Gly	
			100					105					110	1		
C 3 3	000	7 (7)		CITIC	ACT	CTTC	י ייירייי	י ככז								363
					Thr											5.55
GIII	. сту	1115		. val	. 4111	val	120		•							
			,													

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu 10 5 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr 25 20 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 45 40 Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe 55 60 Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn 75 70 Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys 85 90 Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly 105 110 100 Gln Gly Thr Leu Val Thr Val Ser Ala 120 115